RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/537,075_

Source: _PCT/10_

Date Processed by STIC: _6/13/05_

ENTERED

PCT

RAW SEQUENCE LISTING   DATE: 06/13/2005
PATENT APPLICATION: **US/10/537,075** TIME: 09:38:34

Input Set : **A:\12810-91 Sequence Listing.txt**
Output Set: **N:\CRF4\06132005\J537075.raw**

```
 3 <110> APPLICANT: Kesseler, Maria
 4        Zelinski, Thomas
 5        Hauer, Bernhard
 7 <120> TITLE OF INVENTION: L-RHAMNOSE-INDUCIBLE EXPRESSION SYSTEMS
 9 <130> FILE REFERENCE: 12810-00091-US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/537,075
C--> 11 <141> CURRENT FILING DATE: 2005-06-01
11 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/013367
12 <151> PRIOR FILING DATE: 2003-11-27
14 <150> PRIOR APPLICATION NUMBER: DE 102 56 381.0
15 <151> PRIOR FILING DATE: 2002-12-02
17 <160> NUMBER OF SEQ ID NOS: 19
19 <170> SOFTWARE: PatentIn version 3.3
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2046
23 <212> TYPE: DNA
24 <213> ORGANISM: Escherichia coli
26 <220> FEATURE:
27 <221> NAME/KEY: misc_feature
28 <222> LOCATION: (288)..(1121)
29 <223> OTHER INFORMATION: coding for rhaS (positive regulator of rhaBAD operon)
31 <220> FEATURE:
32 <221> NAME/KEY: misc_feature
33 <222> LOCATION: (1108)..(2043)
34 <223> OTHER INFORMATION: coding for rhaR (positive regulator of rhaRS operon)
36 <220> FEATURE:
37 <221> NAME/KEY: protein_bind
38 <222> LOCATION: (56)..(72)
39 <223> OTHER INFORMATION: potential RhaS binding site
41 <220> FEATURE:
42 <221> NAME/KEY: protein_bind
43 <222> LOCATION: (89)..(105)
44 <223> OTHER INFORMATION: potential RhaS binding site
46 <220> FEATURE:
47 <221> NAME/KEY: protein_bind
48 <222> LOCATION: (172)..(203)
49 <223> OTHER INFORMATION: potential RhaR binding site
51 <220> FEATURE:
52 <221> NAME/KEY: protein_bind
53 <222> LOCATION: (210)..(241)
54 <223> OTHER INFORMATION: potential RhaR binding site
56 <220> FEATURE:
57 <221> NAME/KEY: misc_feature
```

```
 58 <222> LOCATION: (24)
 59 <223> OTHER INFORMATION: potential start of transcription (complement)
```
W--> `60 <400> SEQUENCE: 1`
```
 61 aatgtgatcc tgctgaattt cattacgacc agtctaaaaa gcgcctgaat tcgcgacctt 60
 62 ctcgttactg acaggaaaat gggccattgg caaccaggga aagatgaacg tgatgatgtt 120
 63 cacaatttgc tgaattgtgg tgatgtgatg ctcaccgcat ttcctgaaaa ttcacgctgt 180
 64 atcttgaaaa atcgacgttt tttacgtggt tttccgtcga aaatttaagg taagaacctg 240
 65 acctcgtgat tactatttcg ccgtgttgac gacatcagga ggccagtatg accgtattac 300
 66 atagtgtgga ttttttttccg tctggtaacg cgtccgtggc gatagaaccc cggctcccgc 360
 67 aggcggattt tcctgaacat catcatgatt ttcatgaaat tgtgattgtc gaacatggca 420
 68 cgggtattca tgtgtttaat gggcagccct ataccatcac cggtggcacg tctgtttcg 480
 69 tacgcgatca tgatcggcat ctgtatgaac ataccgataa tctgtgtctg accaatgtgc 540
 70 tgtatcgctc gccggatcga tttcagtttc tcgccgggct gaatcagttg ctgccacaag 600
 71 agctggatgg gcagtatccg tctcactggc gcgttaacca cagcgtattg cagcaggtgc 660
 72 gacagctggt tgcacagatg gaacagcagg aaggggaaaa tgatttaccc tcgaccgcca 720
 73 gtcgcgagat cttgtttatg caattactgc tcttgctgcg taaaagcagt ttgcaggaga 780
 74 acctggaaaa cagcgcatca cgtctcaact tgcttctggc ctggctggag gaccattttg 840
 75 ccgatgaggt gaattgggat gccgtggcgg atcaattttc tctttcactg cgtacgctac 900
 76 atcggcagct taagcagcaa acgggactga cgcctcagcg atacctgaac cgcctgcgac 960
 77 tgatgaaagc ccgacatctg ctacgccaca gcgaggccag cgttactgac atcgcctatc 1020
 78 gctgtggatt cagcgacagt aaccactttt cgacgctttt tcgccgagag tttaactggt 1080
 79 caccgcgtga tattcgccag ggacgggatg gctttctgca ataacgcgaa tcttctcaac 1140
 80 gtatttgtac gccatattgc gaataatcaa cttcgttctc tggccgaggt agccacggtg 1200
 81 gcgcatcagt taaaacttct caaagatgat ttttttgcca gcgaccagca ggcagtcgct 1260
 82 gtggctgacc gttatccgca agatgtcttt gctgaacata cacatgattt ttgtgagctg 1320
 83 gtgattgtct ggcgcgggtaa tggcctgcat gtactcaacg atcgccctta tcgcattacc 1380
 84 cgtggcgatc tcttttacat tcatgctgac gataaacact cctacgcttc cgttaacgat 1440
 85 ctggtttttgc agaatattat ttattgcccg gagcgtctga agctgaatct tgactggcag 1500
 86 ggggcgattc cgggatttaa cgccagcgca gggcaaccac actggcgctt aggtagcatg 1560
 87 gggatggcgc aggcgcggca ggttatcggt cagcttgagc atgaaagtag tcagcatgtg 1620
 88 ccgtttgcta acgaaatggc tgagttgctg ttcgggcagt tggtgatgtt gctgaatcgc 1680
 89 catcgttaca ccagtgattc gttgccgcca acatccagcg aaacgttgct ggataagctg 1740
 90 attacccggc tggcggctag cctgaaaagt ccctttgcgc tggataaatt ttgtgatgag 1800
 91 gcatcgtgca gtgagcgcgt tttgcgtcag caatttcgcc agcagactgg aatgaccatc 1860
 92 aatcaatatc tgcgacaggt cagagtgtgt catgcgcaat atcttctcca gcatagccgc 1920
 93 ctgttaatca gtgatatttc gaccgaatgt ggctttgaag atagtaacta tttttcggtg 1980
 94 gtgtttaccc gggaaaccgg gatgacgccc agccagtggc gtcatctcaa ttcgcagaaa 2040
 95 gattaa                                                           2046
 98 <210> SEQ ID NO: 2
 99 <211> LENGTH: 287
100 <212> TYPE: DNA
101 <213> ORGANISM: Escherichia coli
```
W--> `102 <220> FEATURE:`
```
103 <221> NAME/KEY: promoter
104 <222> LOCATION: (1)..(287)
105 <223> OTHER INFORMATION: rhaBAD promoter fragment containing rhaS and rhaR binding
sites
```
W--> `106 <400> SEQUENCE: 2`
```
107 actggcctcc tgatgtcgtc aacacggcga aatagtaatc acgaggtcag gttcttacct 60
108 taaattttcg acggaaaacc acgtaaaaaa cgtcgatttt tcaagataca gcgtgaattt 120
```

Input Set : A:\12810-91 Sequence Listing.txt
Output Set: N:\CRF4\06132005\J537075.raw

```
     109 tcaggaaatg cggtgagcat cacatcacca caattcagca aattgtgaac atcatcacgt 180
     110 tcatctttcc ctggttgcca atggcccatt ttcctgtcag taacgagaag gtcgcgaatt 240
     111 caggcgcttt ttagactggt cgtaatgaaa ttcagcagga tcacatt             287
     114 <210> SEQ ID NO: 3
     115 <211> LENGTH: 125
     116 <212> TYPE: DNA
     117 <213> ORGANISM: Escherichia coli
W--> 118 <220> FEATURE:
     119 <221> NAME/KEY: promoter
     120 <222> LOCATION: (1)..(125)
     121 <223> OTHER INFORMATION: rhaBAD promoter fragment containing RhaS binding site
W--> 122 <400> SEQUENCE: 3
     123 ttgtgaacat catcacgttc atctttccct ggttgccaat ggcccatttt cctgtcagta 60
     124 acgagaaggt cgcgaattca ggcgcttttt agactggtcg taatgaaatt cagcaggatc 120
     125 acatt                                                         125
     128 <210> SEQ ID NO: 4
     129 <211> LENGTH: 123
     130 <212> TYPE: DNA
     131 <213> ORGANISM: Escherichia coli
W--> 132 <220> FEATURE:
     133 <221> NAME/KEY: promoter
     134 <222> LOCATION: (1)..(123)
     135 <223> OTHER INFORMATION: rhaBAD promoter fragment containing RhaS binding site
W--> 136 <400> SEQUENCE: 4
     137 atcaccacaa ttcagcaaat tgtgaacatc atcacgttca tctttccctg gttgccaatg 60
     138 gcccattttc ctgtcagtaa cgagaaggtc gcgaattcag gcgcttttta gactggtcgt 120
     139 aat                                                           123
     142 <210> SEQ ID NO: 5
     143 <211> LENGTH: 51
     144 <212> TYPE: DNA
     145 <213> ORGANISM: Escherichia coli
W--> 146 <220> FEATURE:
     147 <221> NAME/KEY: misc_feature
     148 <222> LOCATION: (1)..(51)
     149 <223> OTHER INFORMATION: palindromic RhaS binding site of rhaBAD promoter
W--> 150 <400> SEQUENCE: 5
     151 atctttccct ggttgccaat ggcccatttt cctgtcagta acgagaaggt c         51
     154 <210> SEQ ID NO: 6
     155 <211> LENGTH: 1071
     156 <212> TYPE: DNA
     157 <213> ORGANISM: Alcaligenes faecalis
W--> 158 <220> FEATURE:
     159 <221> NAME/KEY: CDS
     160 <222> LOCATION: (1)..(1068)
     161 <223> OTHER INFORMATION: coding for nitrilase
W--> 162 <400> SEQUENCE: 6
     163 atg cag aca aga aaa atc gtc cgg gca gcc gcc gta cag gcc gcc tct    48
     164 Met Gln Thr Arg Lys Ile Val Arg Ala Ala Ala Val Gln Ala Ala Ser
     165   1               5                  10                  15
```

```
166 ccc aac tac gat ctg gca acg ggt gtt gat aaa acc att gag ctg gct   96
167 Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala
168             20                  25                  30
169 cgt cag gcc cgc gat gag ggc tgt gac ctg atc gtg ttt ggt gaa acc   144
170 Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr
171         35                  40                  45
172 tgg ctg ccc gga tat ccc ttc cac gtc tgg ctg ggc gca ccg gcc tgg   192
173 Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp
174     50                  55                  60
175 tcg ctg aaa tac agt gcc cgc tac tat gcc aac tcg ctc tcg ctg gac   240
176 Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp
177 65                  70                  75                  80
178 agt gca gag ttt caa cgc att gcc cag gcc gca cgg acc ttg ggt att   288
179 Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile
180                 85                  90                  95
181 ttc atc gca ctg ggt tat agc gag cgc agc ggc ggc agc ctt tac ctg   336
182 Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu
183             100                 105                 110
184 ggc caa tgc ctg atc gac gac aag ggc gag atg ctg tgg tcg cgt cgc   384
185 Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg
186         115                 120                 125
187 aaa ctc aaa ccc acg cat gta gag cgc acc gta ttt ggt gaa ggt tat   432
188 Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr
189     130                 135                 140
190 gcc cgt gat ctg att gtg tcc gac aca gaa ctg gga cgc gtc ggt gct   480
191 Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala
192 145                 150                 155                 160
193 cta tgc tgc tgg gag cat ttg tcg ccc ttg agc aag tac gcg ctg tac   528
194 Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr
195             165                 170                 175
196 tcc cag cat gaa gcc att cac att gct gcc tgg ccg tcg ttt tcg cta   576
197 Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu
198             180                 185                 190
199 tac agc gaa cag gcc cac gcc ctc agt gcc aag gtg aac atg gct gcc   624
200 Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala
201         195                 200                 205
202 tcg caa atc tat tcg gtt gaa ggc cag tgc ttt acc atc gcc gcc agc   672
203 Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser
204     210                 215                 220
205 agt gtg gtc acc caa gag acg cta gac atg ctg gaa gtg ggt gaa cac   720
206 Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu His
207 225                 230                 235                 240
208 aac gcc ccc ttg ctg aaa gtg ggc ggc ggc agt tcc atg att ttt gcg   768
209 Asn Ala Pro Leu Leu Lys Val Gly Gly Gly Ser Ser Met Ile Phe Ala
210             245                 250                 255
211 ccg gac gga cgc aca ctg gct ccc tac ctg cct cac gat gcc gag ggc   816
212 Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu Gly
213             260                 265                 270
214 ttg atc att gcc gat ctg aat atg gag gag att gcc ttc gcc aaa gcg   864
```

```
215 Leu Ile Ile Ala Asp Leu Asn Met Glu Glu Ile Ala Phe Ala Lys Ala
216         275                 280                 285
217 atc aat gac ccc gta ggc cac tat tcc aaa ccc gag gcc acc cgt ctg      912
218 Ile Asn Asp Pro Val Gly His Tyr Ser Lys Pro Glu Ala Thr Arg Leu
219     290                 295                 ·300
220 gtg ctg gac ttg ggg cac cga gac ccc atg act cgg gtg cac tcc aaa      960
221 Val Leu Asp Leu Gly His Arg Asp Pro Met Thr Arg Val His Ser Lys
222 305                 310                 315                 320
223 agc gtg acc agg gaa gag gct ccc gag caa ggt gtg caa agc aag att     1008
224 Ser Val Thr Arg Glu Glu Ala Pro Glu Gln Gly Val Gln Ser Lys Ile
225                 325                 330                 335
226 gcc tca gtc gct atc agc cat cca cag gac tcg gac aca ctg cta gtg     1056
227 Ala Ser Val Ala Ile Ser His Pro Gln Asp Ser Asp Thr Leu Leu Val
228                 340                 345                 350
229 caa gag ccg tct tga                                                 1071
230 Gln Glu Pro Ser
231                 355
234 <210> SEQ ID NO: 7
235 <211> LENGTH: 356
236 <212> TYPE: PRT
237 <213> ORGANISM: Alcaligenes faecalis
238 <400> SEQUENCE: 7
239 Met Gln Thr Arg Lys Ile Val Arg Ala Ala Ala Val Gln Ala Ala Ser
240   1                 5                 10                 15
241 Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala
242                 20                 25                 30
243 Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr
244                 35                 40                 45
245 Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp
246         50                 55                 60
247 Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp
248 65                 70                 75                 80
249 Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile
250                 85                 90                 95
251 Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu
252                 100                 105                 110
253 Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg
254         115                 120                 125
255 Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr
256         130                 135                 140
257 Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala
258 145                 150                 155                 160
259 Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr
260                 165                 170                 175
261 Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu
262                 180                 185                 190
263 Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala
264         195                 200                 205
265 Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser
```

W--> 238 <400> SEQUENCE: 7

VERIFICATION SUMMARY   DATE: 06/13/2005
PATENT APPLICATION: **US/10/537,075**   TIME: 09:38:35

Input Set : **A:\12810-91 Sequence Listing.txt**
Output Set: **N:\CRF4\06132005\J537075.raw**

```
L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:60 M:283 W: Missing Blank Line separator, <400> field identifier
L:102 M:283 W: Missing Blank Line separator, <220> field identifier
L:106 M:283 W: Missing Blank Line separator, <400> field identifier
L:118 M:283 W: Missing Blank Line separator, <220> field identifier
L:122 M:283 W: Missing Blank Line separator, <400> field identifier
L:132 M:283 W: Missing Blank Line separator, <220> field identifier
L:136 M:283 W: Missing Blank Line separator, <400> field identifier
L:146 M:283 W: Missing Blank Line separator, <220> field identifier
L:150 M:283 W: Missing Blank Line separator, <400> field identifier
L:158 M:283 W: Missing Blank Line separator, <220> field identifier
L:162 M:283 W: Missing Blank Line separator, <400> field identifier
L:238 M:283 W: Missing Blank Line separator, <400> field identifier
L:291 M:283 W: Missing Blank Line separator, <220> field identifier
L:295 M:283 W: Missing Blank Line separator, <400> field identifier
L:382 M:283 W: Missing Blank Line separator, <400> field identifier
L:442 M:283 W: Missing Blank Line separator, <220> field identifier
L:446 M:283 W: Missing Blank Line separator, <400> field identifier
L:546 M:283 W: Missing Blank Line separator, <400> field identifier
L:615 M:283 W: Missing Blank Line separator, <220> field identifier
L:619 M:283 W: Missing Blank Line separator, <400> field identifier
L:679 M:283 W: Missing Blank Line separator, <400> field identifier
L:721 M:283 W: Missing Blank Line separator, <220> field identifier
L:725 M:283 W: Missing Blank Line separator, <400> field identifier
L:792 M:283 W: Missing Blank Line separator, <400> field identifier
L:839 M:283 W: Missing Blank Line separator, <220> field identifier
L:843 M:283 W: Missing Blank Line separator, <400> field identifier
L:904 M:283 W: Missing Blank Line separator, <400> field identifier
L:947 M:283 W: Missing Blank Line separator, <220> field identifier
L:951 M:283 W: Missing Blank Line separator, <400> field identifier
L:1024 M:283 W: Missing Blank Line separator, <400> field identifier
```